

A

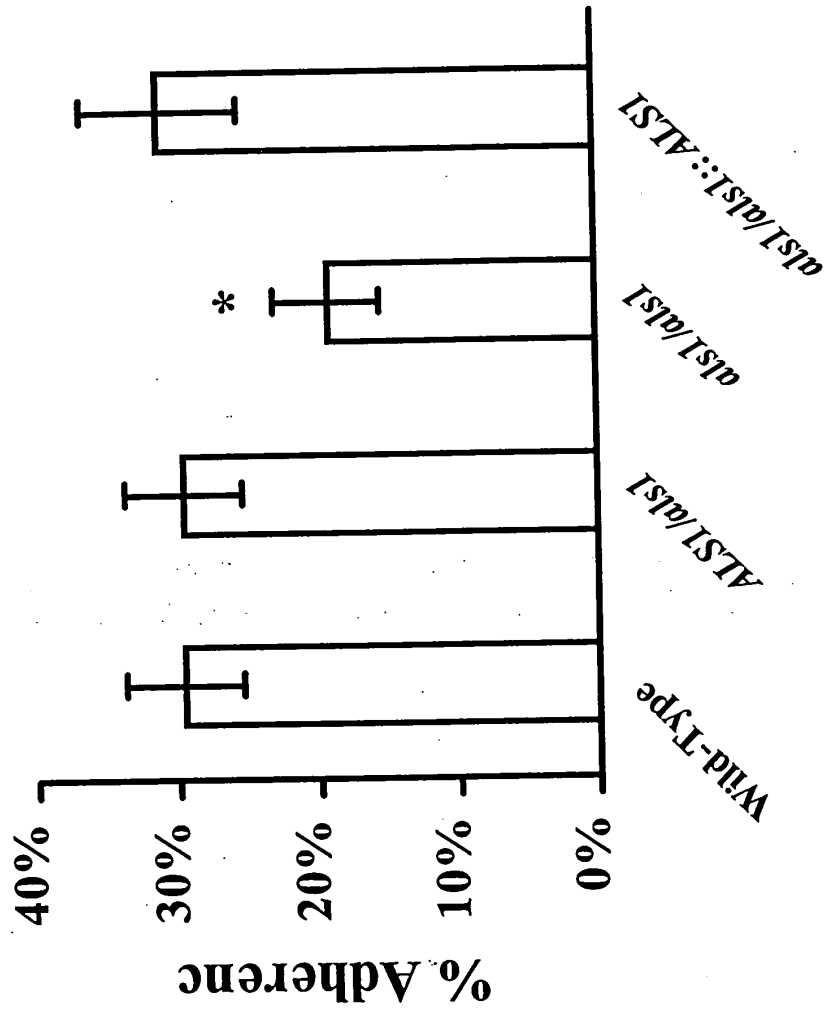


FIGURE 1A

B

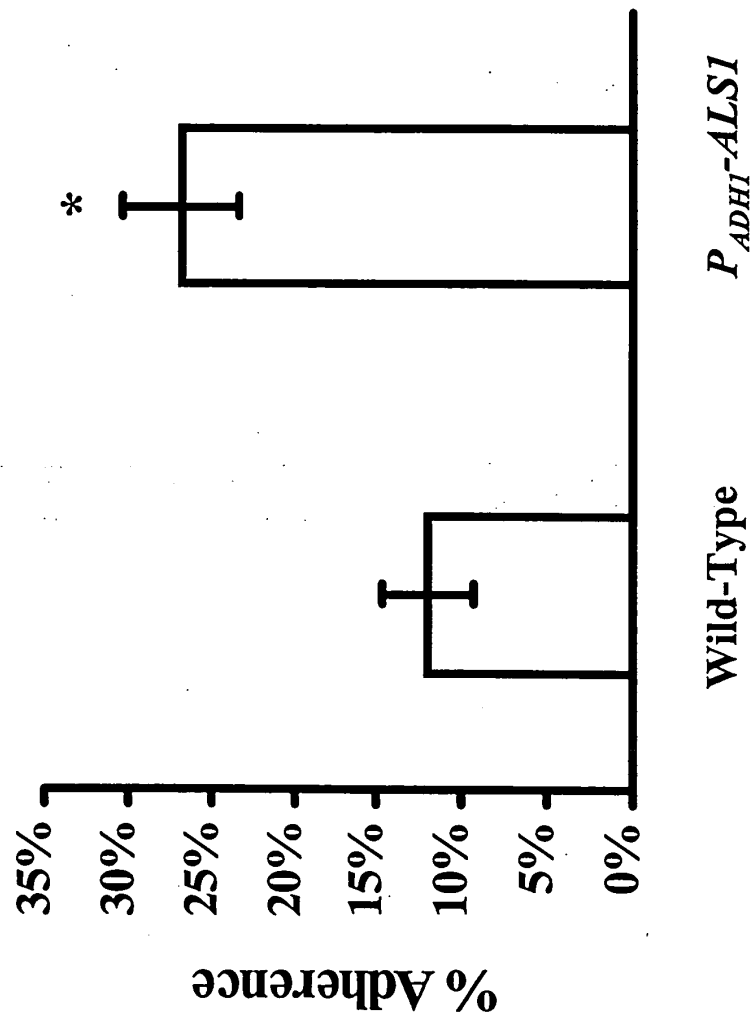


FIGURE 1B

Wild-Type



als1/als1



als1/als1::ALS1

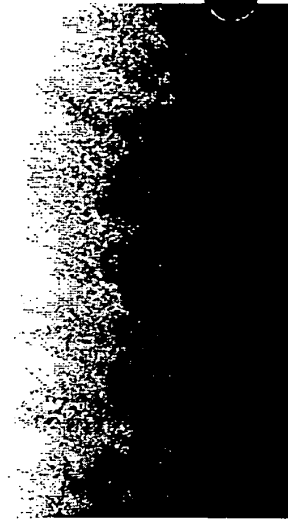


FIGURE 3A

[illegible]

[illegible]

Wild-Type

P_{ADHI}-ALSI

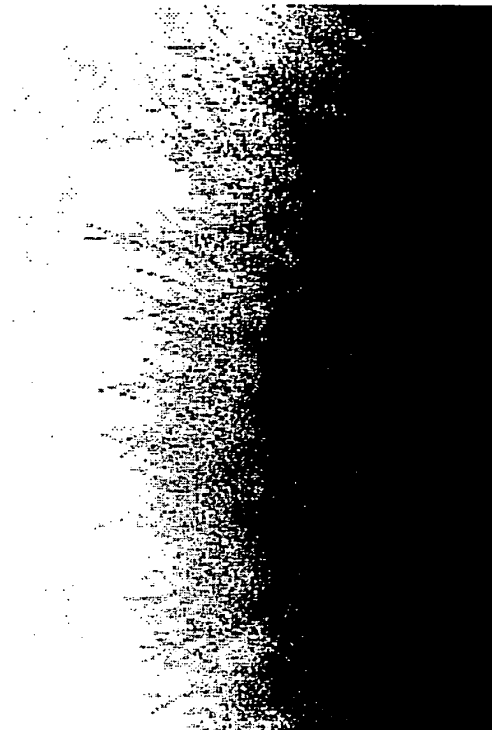
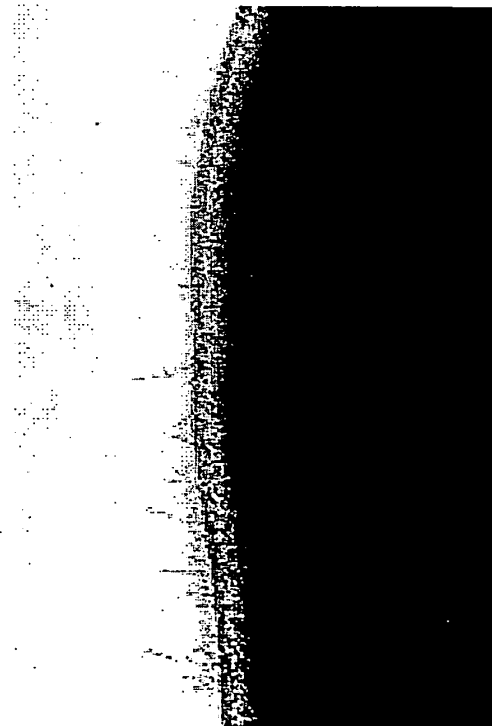


FIGURE 3B

$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{y}} \right) = \frac{\partial L}{\partial y}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{z}} \right) = \frac{\partial L}{\partial z}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\theta}} \right) = \frac{\partial L}{\partial \theta}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\phi}} \right) = \frac{\partial L}{\partial \phi}$
$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\psi}} \right) = \frac{\partial L}{\partial \psi}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\chi}} \right) = \frac{\partial L}{\partial \chi}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\eta}} \right) = \frac{\partial L}{\partial \eta}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\xi}} \right) = \frac{\partial L}{\partial \xi}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\zeta}} \right) = \frac{\partial L}{\partial \zeta}$
$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\delta}} \right) = \frac{\partial L}{\partial \delta}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\epsilon}} \right) = \frac{\partial L}{\partial \epsilon}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\gamma}} \right) = \frac{\partial L}{\partial \gamma}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\beta}} \right) = \frac{\partial L}{\partial \beta}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\alpha}} \right) = \frac{\partial L}{\partial \alpha}$

(a)

Wild-Type

100

Түр

CPH1/efg1

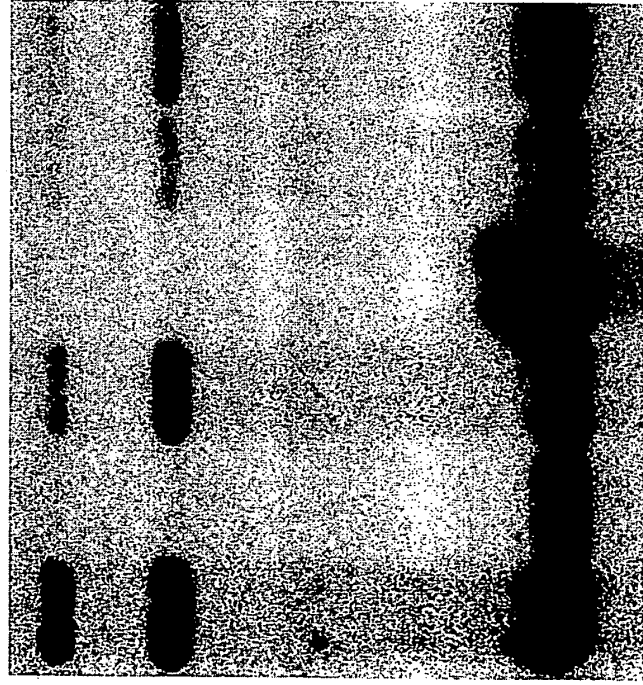
Id m1

Clay

ALSI-2

ALSI-1

ACT1



(a)

Wild-Type

$$18f\partial/18f\partial$$

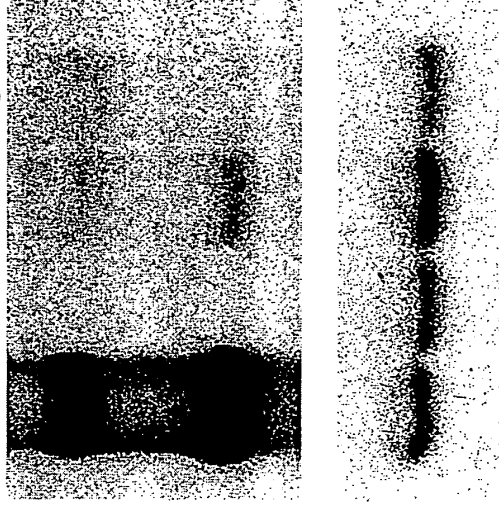
efgi/efgi/efgi

efgI/efgI, P^{ADHI}ALS1

TEFI

ALSI-1

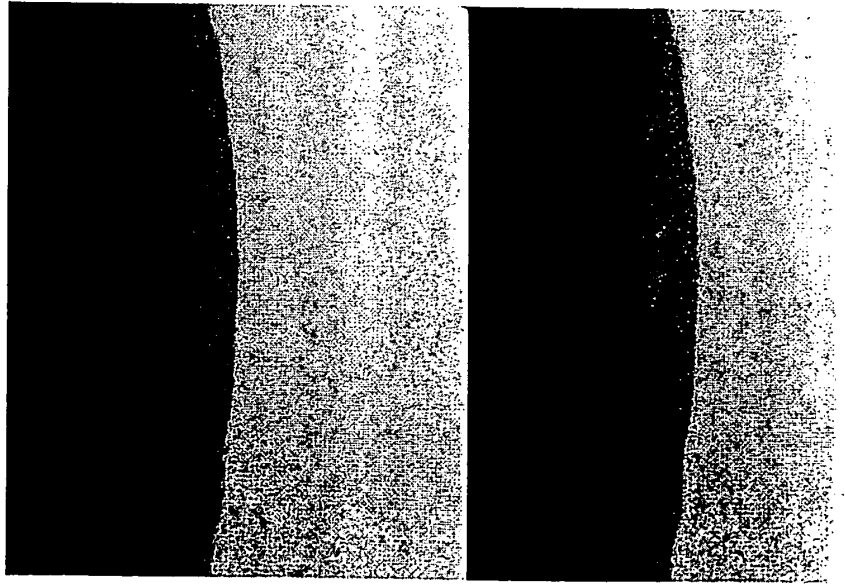
ALSI-2



FINJRES 4A

B

efg1/efg1



efg1/efg1, P_{ADHI} ALS1

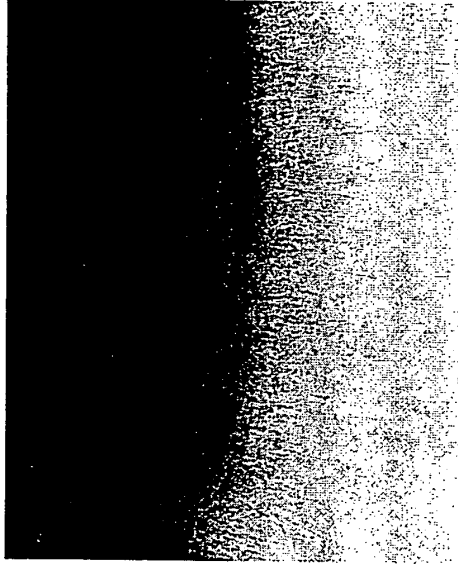


FIGURE 4B

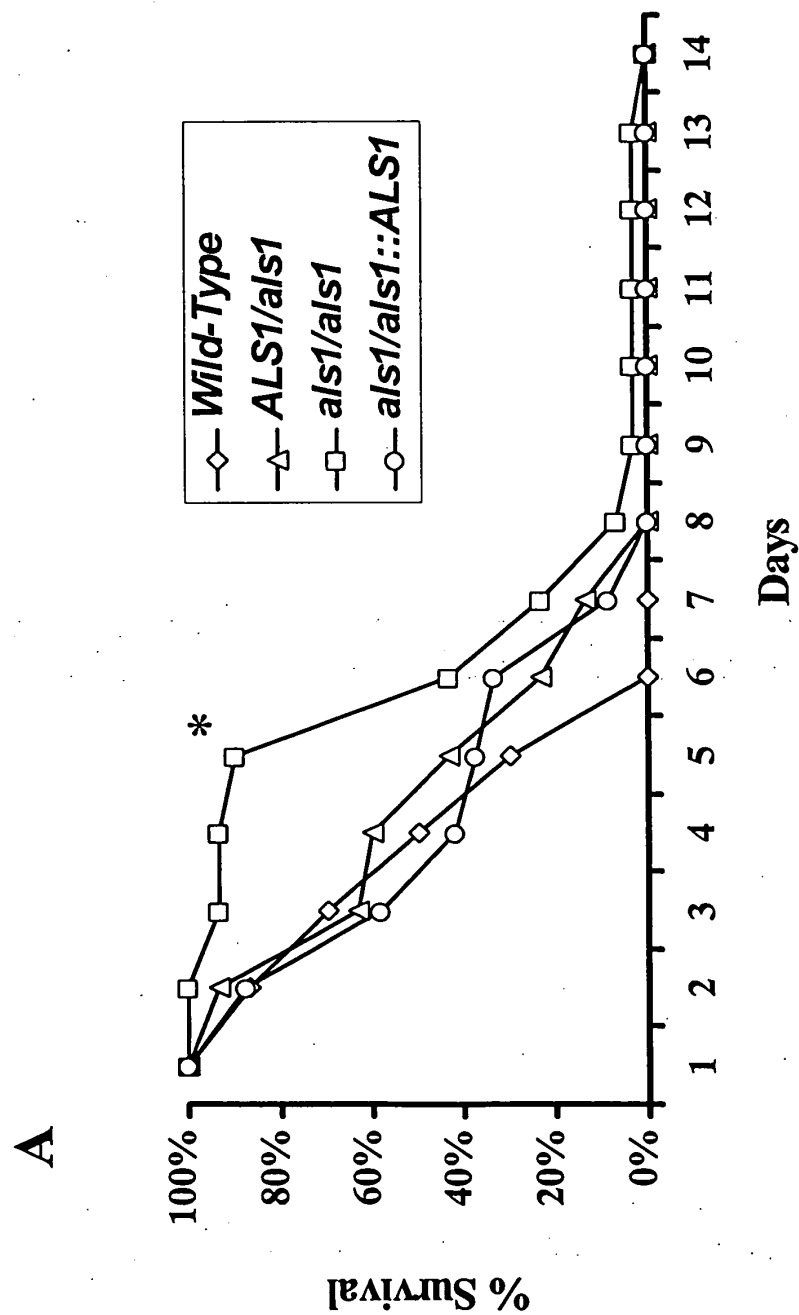


FIGURE 5A

008111-542514200

B

a

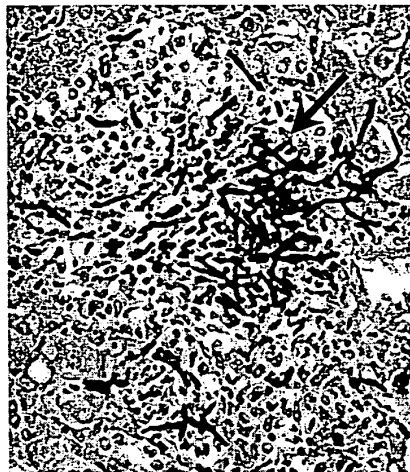
Wild-Type



als1/als1



als1/als1::ALSI



b

Wild-Type



als1/als1



als1/als1::ALSI

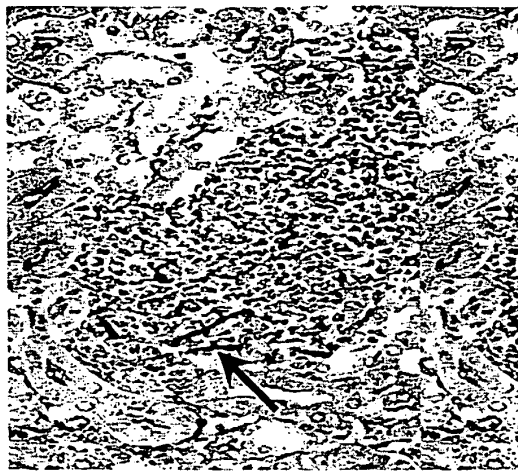
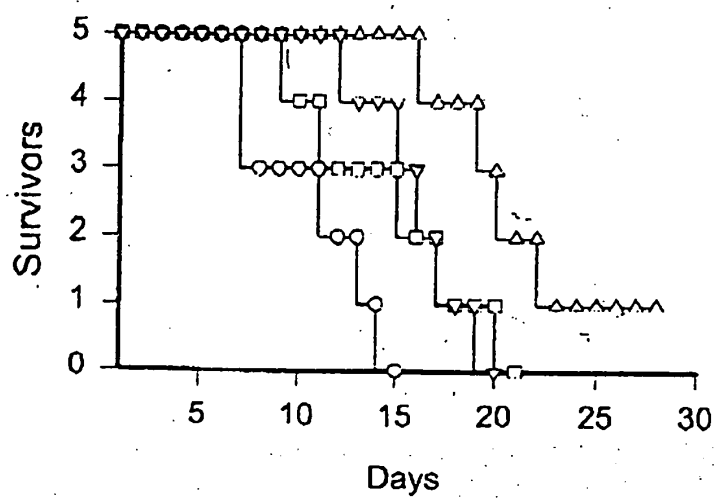


FIGURE 5B

00000-9234200

Prophylactic effect of antiALS antibody against disseminated candidiasis



MST (days)

—○— DPBS	11.4 ± 3.3
—□— NRS (PB) ¹	15.4 ± 4.4
—△— S ² -antiALS	22.0 ± 4.5
—▽— I ³ -antiALS	16.8 ± 2.6

FIGURE 6

0074E82E 44900

1 ATGCTTCAACAATTTACATTGTTATTCCTATATTTGTCAATTGCAAGTGCAAAGACAATC
1 M L Q Q F T L L F L Y L S I A S A K T I
61 ACTGGTGTTTTTGATAGTTTTAATTCATTAACCTGGTCCAATGCTGCTAATTATGCTTTC
21 T G V F D S F N S L T W S N A A N Y A F
121 AAAGGGCCAGGATACCCAACTTGAATGCTGTTTTGGGTGGTCCTTAGATGGTACCAGT
41 K G P G Y P T W N A V L G W S L D G T S
181 GCCAATCCAGGGGATACATTACATTGAATATGCCATGTGTGTTAAATATACTACTTCA
61 A N P G D T F T L N M P C V F K Y T T S
241 CAAACATCTGTTGATTAACTGCCGATGGTGTTAAATATGCTACTTGTCAATTTTATTCT
81 Q T S V D L T A D G V K Y A T C Q F Y S
301 GGTGAAGAATTCACAACTTTTCTACATTAACATGTACTGTGAACGACGCTTTGAAATCA
101 G E E F T T F S T L T C T V N D A L K S
361 TCCATTAAGGCATTTGGTACAGTTACTTTACCAATTGCATTCAATGTTGGTGGAAACAGGT
121 S I K A F G T V T L P I A F N V G G T G
421 TCATCAACTGATTTGGAAGATTCTAAATGTTTTACTGCTGGTACCAATACAGTCACATTT
141 S S T D L E D S K C F T A G T N T V T F
481 AATGATGGTGATAAAGATATCTCAATTGATGTTGAGTTTGAAAAGTCAACCGTTGATCCA
161 N D G D K D I S I D V E F E K S T V D P
541 AGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCAACAACCTTTTTT
181 S A Y L Y A S R V M P S L N K V T T L F
601 GTGGCACCACAATGTGAAAATGGTTACACATCTGGTACAATGGGGTTCTCCAGTAGTAAC
201 V A P Q C E N G Y T S G T M G F S S S N
661 GGTGACGTTGCTATTGATTGCTCAAATATTCATATTGGTATCACAAAAGGATTAAATGAT
221 G D V A I D C S N I H I G I T K G L N D
721 TGAATTATCCGGTTTCATCTGAATCATTTAGTTACACTAAAACCTGTACATCTAATGGA
241 W N Y P V S S E S F S Y T K T C T S N G
781 ATTCAGATTAAATATCAAAATGTACCTGCTGGTTATCGTCCATTTATTGATGCTTATATT
261 I Q I K Y Q N V P A G Y R P F I D A Y I
841 TCTGCTACAGATGTTAACCAATATACTTTAGCATATACCAATGATTATACTTGTGCTGGC
281 S A T D V N Q Y T L A Y T N D Y T C A G
901 AGTCGTCTGCAAAGTAAACCTTTACTTTAAAGATGGACTGGATACAAGAATAGTGATGCC
301 S R L Q S K P F T L R W T G Y K N S D A
961 GGATCTAACGGTATTGTCAATTGTTGCTACAACCTAGAACAGTTACAGACAGTACCCTGCT
321 G S N G I V I V A T T R T V T D S T T A
1021 GTCCTACTTTTACCATTCAATCCAAGTGTGATAAAACCAAAACAATCGAAATTTTGCAA

FIGURE 7

341 V T T L P F N P S V D K T K T I E I L Q
 1081 CCTATTCCAACCACTACCATCACAACTTCATATGTTGGTGTGACTACTTCCTATCTGACT
 361 P I P T T T I T T S Y V G V T T S Y L T
 1141 AAGACTGCACCAATTGGTGAAACAGCTACTGTTATTGTTGATGTGCCATATCATACTACC
 381 K T A P I G E T A T V I V D V P Y H T T
 1201 ACAACTGTTACCAGTGAATGGACAGGAACAATCACTACCACCACAACCTCGTACCAATCCA
 401 T T V T S E W T G T I T T T T T R T N P
 1261 ACTGATTCAATTGACACAGTGGTGGTACAAGTTCCACTGCCAAATCCAACCTGTTAGTACT
 421 T D S I D T V V V Q V P L P N P T V S T
 1321 ACTGAATATTGGTCTCAGTCCTTTGCTACAACCACTACAGTTACTGCTCCTCCAGGTGGT
 441 T E Y W S Q S F A T T T T V T A P P G G
 1381 ACCGATACTGTGATTATCAGAGAGCCACCAACCACTACTGTCACTACTACTGAATATTGG
 461 T D T V I I R E P P N H T V T T T E Y W
 1441 TCACAATCCTTTGCTACTACTACTACTGTTACTGCTCCTCCAGGTGGTACTGACTCAGTA
 481 S Q S F A T T T T V T A P P G G T D S V
 1501 ATTATCAGAGAACCACCAAAATCCAACCTGTCACTACAACCGAGTATTGGTCTCAATCCTTT
 501 I I R E P P N P T V T T T E Y W S Q S F
 1561 GCTACTACTACTACAGTTACTGCTCCTCCAGGTGGTACTGACTCAGTAATTATCAGAGAA
 521 A T T T T V T A P P G G T D S V I I R E
 1621 CCTCCAAACCAACTGTCAACCACTGAATATTGGTCCCAATCTTACGCAACCACAACCT
 541 P P N P T V T T T E Y W S Q S Y A T T T
 1681 ACTGTGACTGCTCCTCCAGGAGGCACTGACTCAGTAATTATCAGAGAACCACCAAAACCAC
 561 T V T A P P G G T D S V I I R E P P N H
 1741 ACTGTCACTACTACTGAATACTGGTCACAATCATATGCCACCACTACCACTGTAACCTGCA
 581 T V T T T E Y W S Q S Y A T T T T V T A
 1801 CCACCAGGTGGTACTGACACTGTTATCATTAGAGAGCCACCAAAACCACACTGTCACTACT
 601 P P G G T D T V I I R E P P N H T V T T
 1861 ACTGAGTATTGGTCTCAATCGTTTGCTACTACCACAACCTGTAACCTGGTCCACCAAGTGGC
 621 T E Y W S Q S F A T T T T V T G P P S G
 1921 ACTGATACTGTTATCATTAGGGAACCACCAAAACCAACTGTCAACCACTACTGAATACTGG
 641 T D T V I I R E P P N P T V T T T E Y W
 1981 TCTCAATCATATGCAACCACTACTACCATTACCGCTCCACCTGGTGAAACTGATACCGTT
 661 S Q S Y A T T T T I T A P P G E T D T V
 2041 CTTATCAGAGAGCCACCAACCACTACTGTCACTACTACTGAATACTGGTCTCAATCATAT
 681 L I R E P P N H T V T T T E Y W S Q S Y
 2101 GCTACAACCACCACTGTTACTGCACCACCTGGTGAAACCGATACCGTTCTTATCAGAGAG
 701 A T T T T V T A P P G E T D T V L I R E
 2161 CCACCAAACCACTACTGTCACTACTACTGAATACTGGTCTCAATCATATGCTACAACCACC

FIGURE 7

721 P P N H T V T T T E Y W S Q S Y A T T T
 2221 ACTGTTACTGCACCACCAGGTGGTACCGATACTGTTATCATTAGAGAGCCACCAAATCCA
 741 T V T A P P G G T D T V I I R E P P N P
 2281 ACAGTTACTACTACTGAATATTGGTCACAATCATTTGCCACAACCACCACAGTTACTGCT
 761 T V T T T E Y W S Q S F A T T T T V T A
 2341 CCTCCAGGTGGTACTGACACTGTGATTATCTATGAAAGCATGTCAAGTTCAAAGATTTCT
 781 P P G G T D T V I I Y E S M S S S K I S
 2401 ACATCCTCCAATGATATAACCAGTATCATTCCATCATTTTCCCGTCCTCATTATGTCAAC
 801 T S S N D I T S I I P S F S R P H Y V N
 2461 AGCACAACCTCCGATTTGTCAACATTTGAATCTTCATCCATGAATACTCCTACTTCTATC
 821 S T T S D L S T F E S S S M N T P T S I
 2521 AGTAGTGATGGTATGTTGTTGTCTTCTACAACCTTTGGTTACTGAATCAGAAACAAC TACA
 841 S S D G M L L S S T T L V T E S E T T T
 2581 GAACTGATTTGCAGTGATGGTAAAGAGTGTCTAGATTGTCCAGTTCTTCTGGTATTGTC
 861 E L I C S D G K E C S R L S S S S G I V
 2641 ACAAATCCAGATAGCAATGAATCCTCAATCGTAACTAGTACTGTTCTCCTACTGCAAGTACA
 881 T N P D S N E S S I V T S T V P T A S T
 2701 ATGTCTGATTCACCTTTCTTCAACTGATGGTATTAGTGCTACATCTTCTGATAATGTTTCA
 901 M S D S L S S T D G I S A T S S D N V S
 2761 AAATCAGGAGTATCAGTTACAACCGAAACTTCTGTTACAAC TATTCAAAC TACTCCAAAC
 921 K S G V S V T T E T S V T T I Q T T P N
 2821 CCATTATCATCTTCAGTGACATCATTGACTCAGTTGTCTTCAATTCCAAGTGTTCAGAA
 941 P L S S S V T S L T Q L S S I P S V S E
 2881 AGTGAAAGTAAAGTTACATTTACAAGCAATGGAGACAACCAAAGTGGTACTCATGATTCA
 961 S E S K V T F T S N G D N Q S G T H D S
 2941 CAATCTACTTCCACTGAAATTGAAATTGTAACAACCAAGTTCTACTAAAGTTTACCACCT
 981 Q S T S T E I E I V T T S S T K V L P P
 3001 GTCGTTTCTTCTAATACTGATTTGACTAGTGAACCAACAAATACCAGAGAACAACCAACT
 1001 V V S S N T D L T S E P T N T R E Q P T
 3061 ACATTATCAACTACTTCAAAC TCCATCACTGAAGATATCACCACATCTCAACCTACAGGT
 1021 T L S T T S N S I T E D I T T S Q P T G
 3121 GATAATGGAGACAATACTTCATCAACCAATCCAGTTCCAAC TGTGGCAACAAGTACTTTA
 1041 D N G D N T S S T N P V P T V A T S T L
 3181 GCATCTGCAAGTGAAGAAGACAACAAAAGCGGTTCTCATGAATCAGCATCCACAAGTTTG
 1061 A S A S E E D N K S G S H E S A S T S L
 3241 AAACCAAGTATGGGTGAAAATTCTGGATTAAC TACTTCTACTGAAATTGAAGCTACAACA
 1081 K P S M G E N S G L T T S T E I E A T T
 3301 ACCAGTCCTACAGAAGCTCCATCACCTGCTGTTTCTTCTGGTACTGATGTAAC TACTGAA

FIGURE 7

1101 T S P T E A P S P A V S S G T D V T T E
 3361 CCAACTGATACTAGAGAACAACCTACTACATTATCAACTACTTCAAAAACAAACAGTGAA
 1121 P T D T R E Q P T T L S T T S K T N S E
 3421 CTGGTTGCTACTACACAAGCTACTAATGAAAATGGTGGTAAATCTCCATCAACTGATTTA
 1141 L V A T T Q A T N E N G G K S P S T D L
 3481 ACATCAAGCTTGACAACAGGCACCTCAGCATCTACAAGTGCTAATAGCGAAGTTGTTACT
 1161 T S S L T T G T S A S T S A N S E L V T
 3541 AGTGGATCTGTTACTGGTGGAGCTGTTGCCAGTGCTTCAAATGATCAATCACATTCTACT
 1181 S G S V T G G A V A S A S N D Q S H S T
 3601 TCTGTTACCAACAGCAACAGCATTGTATCTAATACCCACAAACTACATTGAGTCAACAA
 1201 S V T N S N S I V S N T P Q T T L S Q Q
 3661 GTTACCTCATCCTCACCTTCAACCAACACATTGATTGCTTCTACATACGATGGCTCTGGT
 1221 V T S S S P S T N T F I A S T Y D G S G
 3721 TCTATTATCCAACATTCTACTTGGTTGTACGGTTTGATCACATTATTGTCCTTGTTTCATT
 1241 S I I Q H S T W L Y G L I T L L S L F I
 3781 TAGTGA
 1261 * *

001557
 001558
 001559
 001560
 001561
 001562
 001563
 001564
 001565
 001566
 001567
 001568
 001569
 001570
 001571
 001572
 001573
 001574
 001575
 001576
 001577
 001578
 001579
 001580
 001581
 001582
 001583
 001584
 001585
 001586
 001587
 001588
 001589
 001590
 001591
 001592
 001593
 001594
 001595
 001596
 001597
 001598
 001599
 001600

FIGURE 7